IN THE CLAIMS:

Please amend claims 94, 107, 108, 109, 110, 122, 126 and 127 as follows. Please cancel claims 54-93, 99, 100, 105, 106 and claims 112-126. Please add new claims 127-139.

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94. (Amended) A method of generating a genetic map of an individual, comprising:

(a) providing a polymorphic array comprising three or more single nucleotide polymorphisms (SNPs), wherein each SNP variant in the polymorphic array has an allelic frequency of at least 0.20;

(b) identifying the SNP variants present in an ancestor of the individual by determining the base identity at each SNP site of the ancestor of the individual and identifying the SNP variants present in the individual by determining the base identity at each SNP site of the individual;

(c) determining the number of matches between the individual and the ancestor;

(d) calculating the extent of genetic linkage between each allele from the number of matches of step (c) and the probability that any pair of alleles found in the individual were inherited from the same ancestor based on the allelic frequencies of the SNP variants of the polymorphic array, thereby generating the genetic map of the individual.

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101. (Amended) A method of associating the presence of a particular trait of interest found in a population of individuals with two or more SNP variants, comprising:

(a) selecting two or more SNP sites wherein each of the SNP variants has a known allelic frequency and does not cause the trait;

(b) identifying the SNP variants present in each individual having the trait of interest by determining the base identity at each SNP site, and

(c) determining whether two or more SNP variants are present in the population of individuals having the trait of interest at frequencies greater than the allelic frequency

present in individuals lacking the trait, thus associating the two or more SNP variants with the trait of interest.

102. (Amended) A method according to claim 101, wherein each SNP variant has an allelic frequency of at least 0.20.

107. (Amended) A method according to claims 94 or 101, wherein the individual is selected from the group consisting of animals and plants.

108. (Amended) A method according to claim 107, wherein the individual is a mammal.

109. (Amended) A method according to claim 108, wherein the mammal is selected from the group consisting of human, non-human primates, dogs, cats, cattle, sheep and horses.

110. (Amended) A method according to claim 108, wherein the individual is a human.

111. (Amended) A method according to claim 108, wherein the individual is a horse.

127. (New) A method of associating the presence of a particular SNP variant with a trait of interest found in a population of individuals, comprising:

(a) assembling a polymorphic array from a set of randomly selected SNP variants of known allelic frequencies;

(b) identifying the corresponding alleles present in each individual in the population having the trait of interest by determining the base identity present in these individuals at each SNP site present in the polymorphic array, and

(c) determining whether one or more SNP variants co-segregate with the trait of interest, thus associating the SNP variants with the trait of interest.

128. (New) A method according to claim 127, wherein each SNP variant has an allelic frequency of at least 0.20.

129. (New) A method according to claim 127, further comprising calculating a LOD score and establishing a genetic linkage of SNP variants and the trait of interest.

130. (New) A method according to claim 127, wherein the polymorphic array comprises three or more SNPs.

131. (New) A method according to claim 127, wherein none of the SNP variants in the polymorphic array causes the trait.

132. (New) A method according to claim 127, wherein the polymorphic array comprises
a genetic map.

133. (New) A method of genetic analysis of a set of individuals of the same species comprising:
providing a polymorphic array comprising a set of single nucleotide polymorphisms (SNPs) and determining the presence or absence of the polymorphisms in the set of SNPs in each of the set of individuals and establishing whether the presence or absence of a particular allele, which does not cause the trait, of a polymorphism in the set of SNPs is associated with a particular trait.

134. (New) A method according to claim 133, further comprising
analyzing the frequency of segregation between the SNPs in the set, thereby establishing a genetic map in which the SNPs act as markers.

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135. (New) A method according to claim 133, wherein the SNPs are at multiple unlinked loci.

136. (New) A method according to claim 133, wherein the SNPs are diallelic or triallelic.

137. (New) A method according to claim 133, wherein the trait is a predisposition to a genetic disease.

138. (New) A method according to claim 133, wherein the alleles have an allelic frequency of greater than 0.20.

139. (New) A method according to claim 133, wherein the polymorphic array comprises 3 or more SNPs.

REMARKS

In Reply to the Office Action of November 17, 2000, the claims have been amended to more clearly and specifically describe Applicants' invention. New claims have also been added. Claims 94-98, 101-104, 107-111, and 127-139 are now pending in the application.

Support for these amendments to the claims and the new claims can be found throughout the specification. Genetic mapping, genetic maps, and the association of SNPs with traits are described throughout the specification. Pages 37-38 and 42-45 of the specification, for example, describe genetic mapping and genetic maps. Association of SNPs with traits is described, for example, at pages 42-45. Allelic frequency is discussed throughout the specification. See for example the discussion at pages 41-42 of the specification. No new matter has been added.